



Simulating Spread of Antimicrobial Resistant Bacteria in the Pig Pen try our online tool

Græsbøll, Kaare; Nielsen, Søren S.; Toft, Nils; Christiansen, Lasse Engbo

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Simulating Spread of Antimicrobial Resistant Bacteria in the Pig Pen

- try our online tool.

Kaare Græsbøll^{1,2,*}, Søren S. Nielsen³, Nils Toft¹, Lasse E. Christiansen²

¹ Section for Epidemiology, National Veterinary Institute, Technical University of Denmark

² Department of Applied Mathematics and Computer Science, Technical University of Denmark

³ Department of Large Animal Science, University of Copenhagen, Denmark

Background

Antimicrobial resistance is an increasing challenge. For example, 40% of *Escherichia coli* in Danish pigs are resistant to tetracycline.

The purpose of the MiniResist project is to find treatment protocols that **reduce antimicrobial resistance development**. The project includes a field trial with +2,000 pigs. This poster presents an app that can be used for exploring the effects of different treatment strategies.

Model

The experiments inform a mathematical model that incorporates **multiple pigs and multiple bacterial strains** interacting in a pen.

Antimicrobial (AM) dependent growth of individual bacterial strains in individual pigs is simulated, including dynamic effects of the excretion to and uptake of bacteria from the common pen environment. The model app includes AM treatments where length, dose, and time can be specified by the user.

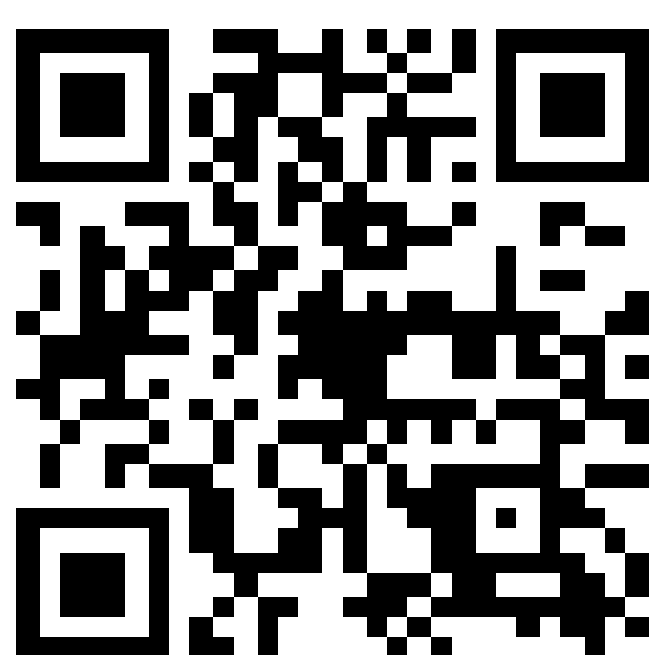
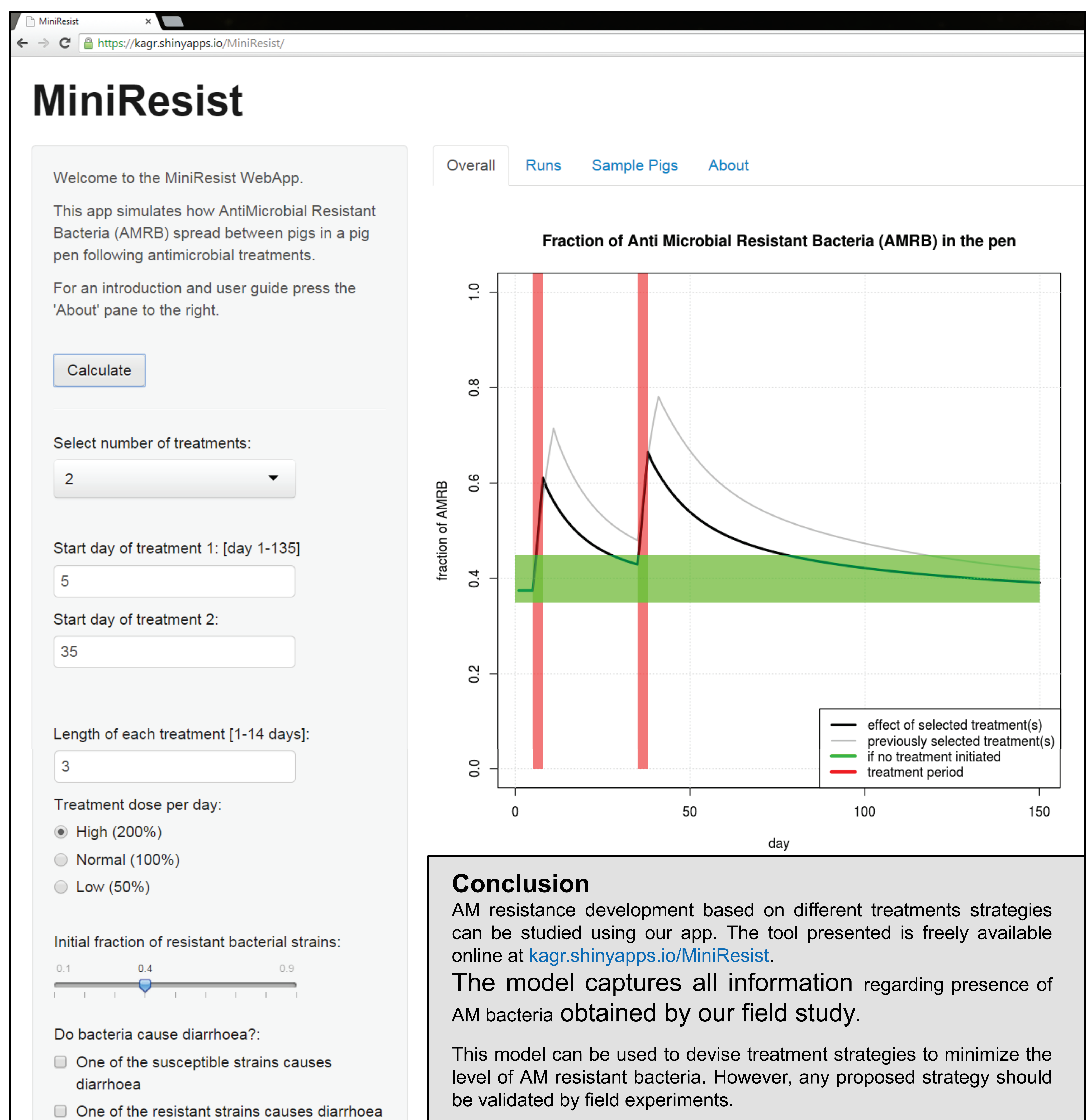
Growth rates of more than 50 *E. coli* strains, collected from Danish farms, were estimated for different AM concentrations to inform the model.

The mathematical model captures the temporal effects of the field studies. The model was then integrated into an **free online WebApp** using shiny and shinyapps in R.

Results

The figure presents how a shorter duration of AM use may reduce the peak fraction of resistant bacteria (compare black to grey line).

Several further results are discussed in our article [1]. I.e. how diarrhea, excretion rates, and transmission rates affect the level of AM resistant bacteria.



Try our online WebApp!

It predicts the level of antimicrobial resistant bacteria based on treatments that you define.

<https://kagr.shinyapps.io/MiniResist/>



Read the article!

The research presented in this poster is published in: [1]

"How Fitness Reduced Antimicrobial Resistant Bacteria Survive and Spread: A Multiple Pig - Multiple Bacterial Strain Model."

PLoS ONE 9(7): e100458. doi:10.1371/journal.pone.0100458

